

From: Fredman, Jeffrey  
Sent: Monday, August 12, 2002 2:31 PM  
To: STIC-Biotech/ChemLib  
Cc: Angell, Jon E  
Subject: FW: Sequence Database Search Request

PLEASE RUSH.

I APPROVE.

Jeff Fredman  
(Eric, I got it the second after I called you)

Point of Contact:  
Mona Smith  
Technical Information Specialist  
CM1 6A01  
Tel: 308-3278

-----Original Message-----

From: Angell, Jon E  
Sent: Monday, August 12, 2002 2:31 PM  
To: Fredman, Jeffrey  
Subject: Sequence Database Search Request

SEARCH REQUEST FORM  
Scientific and Technical Information Center

Examiner# : 78697  
Art Unit : 1635  
Phone Number: 605-1165  
Date: 8/12/02  
Serial Number: 09/786,043  
Mailbox & Bldg/Room Location: CM1-11E12  
Results Format Preferred (circle): Paper

RECEIVED  
AUG 12 2002  
STIC

I would like to have a search performed using the following SEQ. ID NOs. from application : 09/786,043

SEQ ID NO. 1-- nucleic acid seq. (<900nucleotides in length)  
SEQ ID NO. 2-- amino acid seq. (255 amino acids in length)

NOTE: Please reverse transcribe SEQ ID NO:2 into nucleic acid encoding the seq of SEQ ID NO:2.

I would like a standard search of SEQ ID NO.1 and the cDNA encoding SEQ ID NO:2 , AND an oligomer search of the cDNA encoding SEQ ID NO:2 to identify nucleotide oligos encoding at least 10 contiguous amino acids of SEQ ID NO: 2.

Thanks,  
Eric

J. Eric Angell  
Art Unit 1635  
CM1 12D15  
703-605-1165  
mailbox CM1 11E12

Searcher: M. Smith  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/13/02  
Date Completed: 8/14/02  
Searcher Prep/Review: 10  
Clerical: \_\_\_\_\_  
Online time: 15

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 3  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

InterPro: IPR003118; SAM\_PNT.  
 Pfam: PF00178; Ets; 1.  
 PRINTS: PF02198; SAM\_PNT; 1.  
 SMART: SM00454; ETSDOMAIN.  
 SMART: SM00413; ETS; 1.  
 SMART: SM00251; SAM\_PNT; 1.  
 PROSITE: PS50061; ETS\_DOMAIN; 3; 1.  
 SEQUENCE 300 AA; 34893 MW; 51CB66E6195AE06 CRC64;

Query Match 40.7%; Score 574; DB 4; Length 300;  
 Best Local Similarity 41.3%; Pred. No. 2.6e-47;  
 Matches 117; Conservative 47; Mismatches 63; Indels 56; Gaps 8;

22 SMTDLFSNEEYPAPEHQTACDYSYTSVHPYWKRRHWEMLOFCCDOYKLDNTNCISFCN 81  
 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOWTYKQVEMWLOHLDLNDQDASCIPE 77  
 82 FNISGLQCSMTQEEFEVPAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131  
 78 FDISEGHLCMSLOEFTTRAAGAGQLLYENLQHLKMGCCSSDLFQSTHNYIVKTEQTEP 137  
 132 TIND-VADSNCL-----KTSGI-----KSD-----C 152  
 138 SIMNTWKEENYLYDPSYGVLDLDSKTFPCRAQISMTTSHLPVAESPDKKEQDPAPAC 197  
 153 HSRTSLSOSHLMFVRDLILSPENCILWEDEDOGIFRYVKSALAKMGORKKND 212  
 198 HT-KKHNPRGTHLMEFRIDILILSPKNGPLIKWEDSEGFRLKSEAVAOIMGKKKNS 256  
 213 RMYEKLRSALRYKYKTLGLERVD-RRLVYKFGKNAHMGQEDK 254  
 257 SMTYELSRAMRYKYKREILERVGRRLVYKFGKNAHMGRENE 299

## RESULT 12

070273 PRELIMINARY; PRT; 300 AA.

AC 070273  
 DT 01-AUG-1998 (TREMBLrel. 07, Created) *AF055507*  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE EHF.  
 GN Mus.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=PIUTARY;  
 MEDLINE=98262938; PubMed=9600089;  
 ROBERT M. A., Kleinbaum L.A., Sun L.Y., Burton F.H.;  
 "Molecular cloning and expression of Ehf, a new member of the ets  
 transcription factor/oncogene protein gene family.";  
 RL Biochem. Biophys. Res. Commun. 246:176-181(1998).  
 DR HSP: Q00422; IAWC.  
 MGD: MGI:1270840; Ehf.  
 InterPro: IPR000418; Ets.  
 InterPro: IPR002341; HSF\_ETS.  
 Pfam: PF00178; SAM\_PNT.  
 Pfam: PF02198; Ets; 1.  
 PRINTS: PF00454; ETSDOMAIN.  
 SMART: SM00413; ETS; 1.  
 SMART: SM00251; SAM\_PNT; 1.  
 PROSITE: PS50061; ETS\_DOMAIN; 3; 1.  
 SEQUENCE 300 AA; 34903 MW; 91D9477EFB874747 CRC64;

Query Match 40.3%; Score 568; DB 11; Length 300;  
 Best Local Similarity 42.6%; Pred. No. 9.9e-47;  
 Matches 112; Conservative 47; Mismatches 64; Indels 69; Gaps 8;

Matches 120; Conservative 39; Mismatches 69; Indels 54; Gaps 7;

22 SMTDLFSNEEYPAPEHQTACDYSYTSVHPYWKRRHWEMLOFCCDOYKLDNTNCISFCN 81  
 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOWTYKQVEMWLOHLDLNDQDASCIPE 77  
 82 FNISGLQCSMTQEEFEVPAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131  
 78 FDISEGHLCMSLOEFTTRAAGAGQLLYENLQHLKMGCCSSDLFQSTHNYIVKTEQTEP 137  
 121 SPFNDAE-----SKATIKYADSNCLKTSGI-----KSD-----CHS 154  
 138 SIMNTWKEENYLYDPSYGVLDLDSKTFPCRAQISMTTSHLPVAESPDKKEQDPAPAC 197  
 155 HSRT-SLSOSHLMFVRDLILSPENCILWEDEDOGIFRYVKSALAKMGORKKND 213  
 198 HT-KKHNPRGTHLMEFRIDILILSPKNGPLIKWEDSEGFRLKSEAVAOIMGKKKNS 257  
 214 MTEYELSRALRYKYKTLGLERVD-RRLVYKFGKNAHMGQEDK 254  
 258 MTEYELSRAMRYKYKREILERVGRRLVYKFGKNAHMGRENE 299

## RESULT 13

099K12 PRELIMINARY; PRT; 285 AA.

ID 099K12  
 AC 099K12  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE SIMILAR TO ETS HOMOLOGOUS FACTOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC005520; AAH05520.1;  
 DR HSP: Q00422; IAWC.  
 InterPro: IPR000418; Ets.  
 InterPro: IPR002341; HSF\_ETS.  
 Pfam: PF00178; SAM\_PNT.  
 Pfam: PF02198; Ets; 1.  
 PRINTS: PF00454; ETSDOMAIN.  
 SMART: SM00413; ETS; 1.  
 SMART: SM00251; SAM\_PNT; 1.  
 PROSITE: PS50061; ETS\_DOMAIN; 3; 1.  
 SEQUENCE 285 AA; 33225 MW; 91338C527C65955F CRC64;

Query Match 35.5%; Score 514; DB 11; Length 285;  
 Best Local Similarity 39.7%; Pred. No. 1.3e-41;  
 Matches 112; Conservative 37; Mismatches 64; Indels 69; Gaps 8;

22 SMTDLFSNEEYPAPEHQTACDYSYTSVHPYWKRRHWEMLOFCCDOYKLDNTNCISFCN 81  
 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOWTYKQVEMWLOHLDLNDQDASCIPE 77  
 82 FNISGLQCSMTQEEFEVPAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131  
 76 -----OETRAAGSAGQLLYENLQHLKMGCCSSDLFQSTHNYIVKTEQTEP 120  
 121 SPFNDAE-----SKATIKYADSNCLKTSGI-----KSD-----CHS 154  
 123 SIMNTWKEENYLYDPSYGVLDLDSKTFPCRAQISMTTSHLPVAESPDKKEQDPAPAC 197  
 155 HSRT-SLSOSHLMFVRDLILSPENCILWEDEDOGIFRYVKSALAKMGORKKND 213  
 183 HT-KKHNPRGTHLMEFRIDILILSPKNGPLIKWEDSEGFRLKSEAVAOIMGKKKNS 242

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:21:50 ; Search time 88.19 Seconds  
(without alignments)  
500.212 Million cell updates/sec

Title: US-09-786-043-2  
Perfect score: 1409  
Sequence: 1 MLDVHTSTPLPNASFCPL.....DRRLVYKFGNAHGQEDKL 255

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mmc.\*
- 8: sp\_organelle.\*
- 9: sp\_plant.\*
- 10: sp\_rodent.\*
- 11: sp\_virus.\*
- 12: sp\_vertebrate.\*
- 13: sp\_unclassified.\*
- 14: sp\_rvirus.\*
- 15: sp\_bacteriap.\*
- 16: sp\_archaeap.\*
- 17: sp\_mmc.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1409	100.0	255	4	Q95175
2	1409	100.0	265	4	Q96Q13
3	1406	99.8	255	4	Q96Q13
4	1406	99.8	265	4	Q96Q13
5	1338	95.0	253	11	Q921H5
6	1330	94.4	253	11	Q921H5
7	588.5	41.8	277	4	Q95V5
8	584.5	41.5	277	4	Q95V5
9	578	41.0	300	4	Q95V4
10	574	40.7	300	4	Q95V4
11	574	40.7	300	4	Q95V4
12	568	40.3	300	11	Q92F73
13	514.5	36.5	285	11	Q99K12
14	430.5	30.6	371	11	Q35275
15	427.5	30.3	348	4	Q99718
16	422	30.0	371	4	P78545

17	299	21.2	335	4	Q95238
18	297	21.1	325	11	Q9WTP3
19	294.5	20.9	79	11	Q922E8
20	276	19.6	538	5	Q93320
21	262	18.6	463	5	Q19695
22	251.5	17.8	363	5	Q97145
23	234.5	16.6	456	13	Q9W629
24	234	16.6	432	13	Q93425
25	233	16.5	451	13	Q9PU61
26	226	16.0	485	13	Q9W700
27	225.5	16.0	211	11	Q922T6
28	224.5	15.9	490	13	Q9YH24
29	222.5	15.8	455	13	Q919E8
30	222	15.8	463	11	Q920K8
31	220.5	15.6	455	11	Q91XV5
32	220	15.6	414	13	Q9PUL6
33	216.5	15.4	486	11	Q920K7
34	215.5	15.3	462	11	Q920K9
35	214.5	15.2	351	11	Q91YH8
36	214	15.2	420	5	Q17057
37	214	15.2	521	4	Q15725
38	214	15.2	533	4	Q15724
39	214	15.2	581	4	Q15723
40	213	15.1	521	11	Q9JHC8
41	213	15.1	533	11	Q9JHC7
42	213	15.1	581	11	Q9JHD0
43	213	15.1	593	11	Q9JHC9
44	211	15.0	279	5	Q9GZK0
45	208.5	14.8	336	6	Q62804

ALIGNMENTS

RESULT 1

Q95175 PRELIMINARY: PRT; 255 AA.  
AC Q95175  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE E74-LIKE FACTOR 5.  
GN ELFS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99054671; PubMed=9840936;  
RA Zhou J., Ng A.Y., Tyms M.J., Jermiin L.S., Seth A.K., Thomas R.S.,  
RA Kola I.;  
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of  
RT ETS genes and maps to human chromosome 11p13-15, a region subject to  
RT LOH and rearrangement in human carcinoma cell lines.";  
RL Oncogene 17:2719-2732(1998).  
DR EMBL; AF049703; AAC79755.1;  
DR HSSP; Q00422; IAWC.  
DR InterPro; IPR000418; ETS.  
DR InterPro; IPR002341; HSF-ETS.  
DR InterPro; IPR003118; SAM\_PNT.  
DR Pfam; PF00178; Ets; 1.  
DR Pfam; PF02198; SAM\_PNT; 1.  
DR PRINTS; PR00454; ETSDOMAIN.  
DR SMART; SM00413; ETS; 1.  
DR SMART; SM00251; SAM\_PNT; 1.  
DR PROSITE; PS00061; ETS\_DOMAIN\_3; 1.  
SQ SEQUENCE 255 AA; 30121 MW; AE61C5B178ECB55 CRC64;

Query Match 100.0%; Score 1409; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 6.1e-128;  
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 60  
 DB 1 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 60  
 QY 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120  
 DB 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120  
 QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180  
 DB 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180  
 QY 181 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240  
 DB 181 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240  
 QY 241 YKFGKNAHGWQEDKL 255  
 DB 241 YKFGKNAHGWQEDKL 255  
 RESULT 2  
 Q96QY3  
 ID Q96QY3 PRELIMINARY; PRT; 265 AA.  
 AC Q96QY3  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE DJ59419.1 (E74-LIKE FACTOR 5 (ETS DOMAIN TRANSCRIPTION  
 DE FACTOR)).  
 GN ELF5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Thomas D.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ALI37224; CAC48256.1;  
 SQ SEQUENCE 265 AA; 31263 MW; 43821A79A45768FE CRC64;

Query Match 100.0%; Score 1409; DB 4; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-128;  
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 60  
 DB 11 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 70  
 QY 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120  
 DB 71 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 130  
 QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180  
 DB 131 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 190  
 QY 181 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240  
 DB 191 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 250  
 QY 241 YKFGKNAHGWQEDKL 255  
 DB 251 YKFGKNAHGWQEDKL 265  
 RESULT 3  
 Q9UKW5  
 ID Q9UKW5 PRELIMINARY; PRT; 255 AA.  
 AC Q9UKW5

DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE ETS TRANSCRIPTION FACTOR ESE-2B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oettgen P., Kas K., Dube A., Gu X., Grall F., Thamrongsak U.,  
 RA Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C.,  
 RA Libermann T.A.;  
 RT "Characterization of ESE-2, a novel ESE-1-related Ets transcription  
 RT factor that is restricted to glandular epithelium and differentiated  
 RT keratinocytes".  
 RL J. Biol. Chem. 274:29439-29452(1999).  
 DR EMBL; AF115403; AAD22961.1;  
 DR HSP; 000422; IAWC.  
 DR InterPro; IPR000418; Ets.  
 DR InterPro; IPR002341; HSF\_ETS.  
 DR InterPro; IPR003118; SAM\_PNT.  
 DR Pfam; PF001178; Ets; 1.  
 DR PRINTS; PF021198; SAM\_PNT; 1.  
 DR SMART; SM00413; ETS; 1.  
 DR SMART; SM00251; SAM\_PNT; 1.  
 DR PROSITE; PS00061; ETS\_DOMAIN\_3; 1.  
 SQ SEQUENCE 255 AA; 30153 MW; 5F71C5B178ECB548 CRC64;  
 Query Match 99.8%; Score 1406; DB 4; Length 255;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-127;  
 Matches 254; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 60  
 DB 1 MLDVTHSTFLPNASFCDFPLMSWTLDFSNEEYYPFAFEHQTACDSYWTSVHPPEYTKRHVV 60  
 QY 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120  
 DB 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120  
 QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180  
 DB 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180  
 QY 181 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240  
 DB 181 GILEWEDREOGIFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240  
 QY 241 YKFGKNAHGWQEDKL 255  
 DB 241 YKFGKNAHGWQEDKL 255  
 RESULT 4  
 Q9UKW6  
 ID Q9UKW6 PRELIMINARY; PRT; 265 AA.  
 AC Q9UKW6  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE ETS TRANSCRIPTION FACTOR ESE-2A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oettgen P., Kas K., Dube A., Gu X., Grall F., Thamrongsak U.,

```

RA Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C.,
RA Libermann T.A.;
RT "Characterization of ESE-2, a novel ESE-1-related Ets transcription
RT factor that is restricted to glandular epithelium and differentiated
RT keratinocytes.";
RL J. Biol. Chem. 274:29439-29452(1999).
DR EMBL; AF115402; AAD22960.1; -.
DR HSSP; Q00422; IAWC.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ET5.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS00661; ETS_DOMAIN_3; 1.
SQ SEQUENCE 265 AA; 31295 MW; B2921A79A45768E3 CRC64;

Query Match 99.8%; Score 1406; DB 4; Length 265;
Best Local Similarity 99.6%; Pred. No. 1.2e-127;
Matches 254; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 60
Db 11 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 70

QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120
Db 71 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 130

QY 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 180
Db 131 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 190

QY 181 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 240
Db 191 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 250.

QY 241 YKFGKNAHGWOEDKL 255
Db 251 YKFGKNAHGWOEDKL 265

RESULT 5
Q921H5 PRELIMINARY; PRT; 253 AA.
AC Q921H5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE SIMILAR TO E74-LIKE FACTOR 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012424; AAH12424.1; -.
SQ SEQUENCE 253 AA; 29872 MW; 3FC4799F77AFCF48 CRC64;

Query Match 95.0%; Score 1338; DB 11; Length 253;
Best Local Similarity 94.5%; Pred. No. 4.2e-121;
Matches 241; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 60
Db 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 60

QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120
Db 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120

QY 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 180
Db 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 178

QY 181 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 240
Db 179 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 238

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QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120
Db 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120

QY 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 180
Db 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 178

QY 181 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 240
Db 179 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 238

QY 241 YKFGKNAHGWOEDKL 255
Db 239 YKFGKNAHGWOEDKL 253

RESULT 6
Q922K6 PRELIMINARY; PRT; 253 AA.
AC Q922K6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE E74-LIKE FACTOR 5.
GN ELF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou J., Ng A.Y., Tyms M.J., Jermlin L.S., Seth A.K., Thomas R.S.,
RA Kola I.;
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
RT ETS genes and maps to human chromosome 11p13-15, a region subject to
RT LOH and rearrangement in human carcinoma cell lines.";
RL Oncogene 17:2719-2732(1998).
DR EMBL; AF049702; AAC79754.1; -.
DR HSSP; Q00422; IAWC.
DR MGD; MGI:1335079; Elf5.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ET5.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS00661; ETS_DOMAIN_3; 1.
SQ SEQUENCE 253 AA; 29971 MW; 3FD028DA77AFCF48 CRC64;

Query Match 94.4%; Score 1330; DB 11; Length 253;
Best Local Similarity 94.1%; Pred. No. 2.5e-120;
Matches 240; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 60
Db 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHQACDSYWTSVHPYWKRRHV 60

QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120
Db 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQBEFVEAAGLCGEYLYFILONIRTOGY 120

QY 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 180
Db 121 SFFNDAESKATIKDYADNSCLKTSGIKSQDCHSHSRSTSLOSSHLMFEFVRDRLV 178

QY 181 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 240
Db 179 GILEWEDREQIGFRVVKSEALAKMWGQKKNDRMTYEKLSRALRYYYKTYGILERVDRRLV 238

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RESULT	8
Q9H509	
ID	Q9H509
AC	PRELIMINARY;
Q9H509;	PRT; 277 AA.
01-MAR-2001	(TrEMBLrel. 16, Created)
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RC	TISSUE=PROSTATE GLAND;
RX	MEDLINE=20112875; PubMed=10644770;
RA	Kas K., Finger E., Grall F., Gu X., Akbarali Y., Boltax J., Weiss A.,
RA	Oettgen P., Kapeller R., Libermann T.A.;
RT	"ESE-3, a Novel Member of an Epithelium-specific Ets Transcription
RT	Factor Subfamily, Demonstrates Different Target Gene Specificity from

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RT ESE-1."
RL J. Biol. Chem. 275:2986-2998(2000).
DR EMBL; AF124439; AAD30991.1; -
DR HSSP; Q00422; 1AWC.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETs.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS0061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 300 AA; 34920 MW; 3DEC66577780FEC1 CRC64;

Query Match 41.0%; Score 578; DB 4; Length 300;
Best Local Similarity 41.7%; Pred. No. 1.le-47;
Matches 118; Conservative 47; Mismatches 62; Indels 56; Gaps 8;

QY 22 SWTDLFSNEEYPAFEHOTACDSYVTSVHPEYTKRHWEMWLFQCCDQYKLDNTNCISFCN 81
DB 23 AWTDSYTCNVSSGF-----FGSQWHEIHPOYTKYQVWEMWLFQCCDQYKLDNTNCISFCN 77
QY 82 FNISGLQSCMTQEEFVEAAGLGGYLYFILLQNTQCG-----YSFNDAAESKA 131
DB 78 FDINGEHLCSMSLOEFFTRAAGTAGOLLYSNLQHLKWNQCCSDLFQSTHNIVVTKTEQTEP 137
QY 132 TKID-YADSNCL-----KTSGI-----KSQD-----C 152
DB 138 SIMNTWKDENLYDTNGYSTVDLLDGKTCFRCVQISMTTSHLPVAESPDMKKEODPPAKC 197
QY 153 HSHSRTSLQSSHLWFEVVDLLSPENGILWEDREGIFRVYKSEALAKMWGQKKN 212
DB 198 HT-KKHNPGRGTHLWFEVVDLLSPENGILWEDREGIFRVYKSEALAKMWGQKKN 256
QY 213 RMTYEKLSRALRYKYGKILERVDRVRLVYKFGKNAHQWQEDK 254
DB 257 SMTYEKLSRAMRYKRYKREILERVDRGLVYKFGKNAHQWRENE 299

RESULT 10
Q9NZC4 Q9NZC4 PRELIMINARY; PRT; 300 AA.
AC Q9NZC4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ETS DOMAIN TRANSCRIPTION FACTOR (DJ875K15.1.2).
GN ESEJ OR EHF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA BROOKS-WILSON A.R., Buckler A., Cardon L., Carey A.H., Galvin M.,
RA Miller A., North M.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Tugores A., Le J., Sorokina I., Snijders A.J., Duyao' M., Reddy P.S.,
RA Mushagian A., Carlee L., Watanaskul T., Chu S., Emtage S.,
RA McCormick M.K.;
RT "A Novel Epithelial Specific ETS Transcription Factor, ESEJ, is a
RT Negative Modulator of MAP Kinase Signaling Pathways, and its
RT Expression is Lost in Carcinomas."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]

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RP SEQUENCE FROM N.A.
RA Mitchell S.C., Levin E., Hubert R., Yeramian C., Saffran D.C.,
RA Afar D.E.H.;
RT "Up-Regulation of the Epithelial-Specific Transcription Factor Genes
RT hEHF and ESX in Advanced Prostate Cancer.";
RL Prostate 0:0-0(1999).
DR EMBL; AF212848; AAF61670.1; -
DR EMBL; AL157952; CAC12701.1; -
DR EMBL; AF203977; AAG35644.1; -
DR HSSP; Q00422; 1AWC.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETs.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS0061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 300 AA; 34892 MW; 5CABB38BAF852ED0 CRC64;

Query Match 40.7%; Score 574; DB 4; Length 300;
Best Local Similarity 41.3%; Pred. No. 2.6e-47;
Matches 117; Conservative 47; Mismatches 63; Indels 56; Gaps 8;

QY 22 SWTDLFSNEEYPAFEHOTACDSYVTSVHPEYTKRHWEMWLFQCCDQYKLDNTNCISFCN 81
DB 23 AWTDSYTCNVSSGF-----FGSQWHEIHPOYTKYQVWEMWLFQCCDQYKLDNTNCISFCN 77
QY 82 FNISGLQSCMTQEEFVEAAGLGGYLYFILLQNTQCG-----YSFNDAAESKA 131
DB 78 FDINGEHLCSMSLOEFFTRAAGTAGOLLYSNLQHLKWNQCCSDLFQSTHNIVVTKTEQTEP 137
QY 132 TKID-YADSNCL-----KTSGI-----KSQD-----C 152
DB 138 SIMNTWKDENLYDTNGYSTVDLLDGKTCFRCVQISMTTSHLPVAESPDMKKEODPPAKC 197
QY 153 HSHSRTSLQSSHLWFEVVDLLSPENGILWEDREGIFRVYKSEALAKMWGQKKN 212
DB 198 HT-KKHNPGRGTHLWFEVVDLLSPENGILWEDREGIFRVYKSEALAKMWGQKKN 256
QY 213 RMTYEKLSRALRYKYGKILERVDRVRLVYKFGKNAHQWQEDK 254
DB 257 SMTYEKLSRAMRYKRYKREILERVDRGLVYKFGKNAHQWRENE 299

RESULT 11
Q9UKF9 Q9UKF9 PRELIMINARY; PRT; 300 AA.
AC Q9UKF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ETS HOMOLOGOUS FACTOR.
GN EHF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TUGORES A., Le J., Sorokina I., Snijders A.J., Duyao' M., Reddy P.S.,
RA Mushagian A., Carlee L., Watanaskul T., Chu S., Emtage S.,
RA McCormick M.K.;
RT "A Novel Epithelial Specific ETS Transcription Factor, ESEJ, is a
RT Negative Modulator of MAP Kinase Signaling Pathways, and its
RT Expression is Lost in Carcinomas."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]

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Qy 247 AHGWQEDKL 255  
: | : | : :  
Db 358 SSGWKEEV 366

QY	210	KND	R	M	T	Y	E	K	S	R	A	L	R	Y	Y	K	T	G	I	L	E	R	V	D	-	R	R	L	V	Y	K	F	G	K	N	A	H	G	Q	E	D	K	L	255		
Db	297	K	N	S	N	M	T	Y	E	K	S	R	A	M	R	Y	Y	K	K	R	E	I	L	E	R	V	D	G	R	R	L	V	Y	K	F	G	K	N	S	S	G	K	E	E	V	343

Search completed: August 13, 2002, 21:31:15  
Job time: 565 sec

